

## SEQUENCE LISTING

<110> Jensen, Michael

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<223> Human Wild-type Inosine Monophosphate Dehydrogenase  
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<301> Collart, F.R. and Huberman, E.

<302> Cloning and sequence analysis of the human and

<303> J. Biol. Chem. (1988)

<304> 263

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 <301> Farazi et al.  
 <303> J. Biol. Chem. (1997)  
 <304> 271





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ctg Leu 260	gac Asp	ttg Leu	ctc Leu	gcc Ala	cag Gln 265	gct Ala	ggg Gly	gtg Val	gat Asp	gta Val 270	gtg Val	gtt Val	ttg Leu	gac Asp	tct Ser 275	872
tcc Ser	cgg Arg	gga Gly	aat Asn 280	tcc Ser	atc Ile	ttc Phe	cag Gln	atc Ile	aat Asn 285	atg Met	atc Ile	aag Lys	tac Tyr	atc Ile 290	aaa Lys	920
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gcc Ala	cag Gln 310	gcc Ala	aag Lys	aac Asn	ctc Leu	att Ile	gat Asp 315	gca Ala	ggg Gly	gtg Val	gat Asp	gcc Ala 320	ctg Leu	cgg Arg	gtg Val	1016
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 Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg  
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 Asp Val Phe Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile  
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Glu Ala Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln
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Asp Lys Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile
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Gln His Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg
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<300>
<301> Farazi et al.
<303> J. Biol. Chem. (1997)
<304> 272
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<300>
<301> Farazi et al.
<302> Isolation and Characterization of Mycophenolic
<303> J. Biol. Chem. (1997)
<304> 272
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Gln	Asp	Thr	Lys	Leu	Ser	Glu	Ala	Asn	Lys	Ile	Ile	Trp	Glu	Lys	Lys	
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Asp	Ser	Tyr	Val	Pro	Tyr	Ala	Gly	Lys	Leu	Lys	Asp	Asn	Val	Glu	Ala	
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Gln Arg Tyr Asp Leu Gly Gly Lys Gln Lys Leu Ser Phe Glu Glu Gly
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 <303> J. Biol. Chem. (1990)  
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Lys	Tyr	Arg	Leu	Asp	Leu	Leu	Thr	Gln	Ala	Gly	Val	Asp	Val	Ile	Val	
			260					265					270			
ttc	cac	tcg	tcc	caa	ggg	aat	tcg	gtg	tat	cag	atc	gcc	atg	gtg	cat	1464
Phe	His	Ser	Ser	Gln	Gly	Asn	Ser	Val	Tyr	Gln	Ile	Ala	Met	Val	His	
		275					280					285				
tac	atc	aaa	cag	aag	tac	ccc	cac	ctc	cag	gtg	att	ggg	ggg	aac	gtg	1512
Tyr	Ile	Lys	Gln	Lys	Tyr	Pro	His	Leu	Gln	Val	Ile	Gly	Gly	Asn	Val	
	290					295					300					
gtg	aca	gca	gcc	cag	gcc	aag	aac	ctg	att	gat	gct	ggg	gtg	gac	ggg	1560
Val	Thr	Ala	Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	Asp	Gly	
	305				310					315					320	
ctg	cgc	gtg	ggc	atg	ggc	tgc	ggc	tcc	atc	tgc	atc	acc	cag	gaa	gtg	1608
Leu	Arg	Val	Gly	Met	Gly	Cys	Gly	Ser	Ile	Cys	Ile	Thr	Gln	Glu	Val	
				325					330					335		
atg	gcc	tgt	ggg	cgg	ccc	cag	ggc	act	gct	gtg	tac	aag	gtg	gct	gag	1656
Met	Ala	Cys	Gly	Arg	Pro	Gln	Gly	Thr	Ala	Val	Tyr	Lys	Val	Ala	Glu	
			340					345					350			
tat	gcc	cgg	cgc	ttt	ggg	gtg	ccc	atc	ata	gcc	gat	ggc	ggc	atc	cag	1704
Tyr	Ala	Arg	Arg	Phe	Gly	Val	Pro	Ile	Ile	Ala	Asp	Gly	Gly	Ile	Gln	
		355					360					365				
acc	gtg	gga	cac	gtg	gtc	aag	gcc	ctg	gcc	ctt	gga	gcc	tcc	aca	gtg	1752
Thr	Val	Gly	His	Val	Val	Lys	Ala	Leu	Ala	Leu	Gly	Ala	Ser	Thr	Val	
	370					375					380					
atg	atg	ggc	tcc	ctg	ctg	gcc	gcc	act	acg	gag	gcc	cct	ggc	gag	tac	1800
Met	Met	Gly	Ser	Leu	Leu	Ala	Ala	Thr	Thr	Glu	Ala	Pro	Gly	Glu	Tyr	
	385				390					395					400	
ttc	ttc	tca	gac	ggg	gtg	cgg	ctc	aag	aag	tac	cgg	ggc	atg	ggc	tca	1848



Phe	Phe	Ser	Asp	Gly	Val	Arg	Leu	Lys	Lys	Tyr	Arg	Gly	Met	Gly	Ser		
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ctg	gat	ccc	atg	gag	aag	agc	agc	agc	agc	cag	aaa	cga	tac	ttc	agc		1896
Leu	Asp	Pro	Met	Glu	Lys	Ser	Ser	Ser	Ser	Gln	Lys	Arg	Tyr	Phe	Ser		
			420					425					430				
gag	ggg	gat	aaa	gtg	aag	atc	gca	cag	ggg	gtc	tcg	ggc	tcc	atc	cag		1944
Glu	Gly	Asp	Lys	Val	Lys	Ile	Ala	Gln	Gly	Val	Ser	Gly	Ser	Ile	Gln		
			435				440					445					
gac	aaa	gga	tcc	att	cag	aag	ttc	gtg	ccc	tac	ctc	ata	gca	ggc	atc		1992
Asp	Lys	Gly	Ser	Ile	Gln	Lys	Phe	Val	Pro	Tyr	Leu	Ile	Ala	Gly	Ile		
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Gln	His	Gly	Cys	Gln	Asp	Ile	Gly	Ala	Arg	Ser	Leu	Ser	Val	Leu	Arg		
465					470				475						480		
tcc	atg	atg	tac	tca	gga	gag	ctc	aag	ttt	gag	aag	cgg	acc	atg	tcg		2088
Ser	Met	Met	Tyr	Ser	Gly	Glu	Leu	Lys	Phe	Glu	Lys	Arg	Thr	Met	Ser		
				485				490						495			
ccc	cag	att	gag	ggg	ggg	gtc	cat	ggc	ctg	cac	tct	tac	gaa	aag	cgg		2136
Pro	Gln	Ile	Glu	Gly	Gly	Val	His	Gly	Leu	His	Ser	Tyr	Glu	Lys	Arg		
			500					505					510				
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Leu	Tyr																
cactttttggg	cacaggctcc	ctccataact	gagtggtcca	cagatttgca	ctacgggttc												2252
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cgagaccagc	cagccaggct	ctcaggacct	gcgctgcctt	aggatctttc	ttgctgcagc												2432
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 Asn Asp Phe Leu Ile Leu Pro Gly Phe Ile Asp Phe Ile Ala Asp Glu  
 35 40 45  
 Val Asp Leu Thr Ser Ala Leu Thr Arg Lys Ile Thr Leu Lys Thr Pro  
 50 55 60  
 Leu Ile Ser Ser Pro Met Asp Thr Val Thr Glu Ala Asp Met Ala Ile  
 65 70 75 80  
 Ala Met Ala Leu Met Gly Gly Ile Gly Phe Ile His His Asn Cys Thr  
 85 90 95

Pro	Glu	Phe	Gln	Ala	Asn	Glu	Val	Arg	Lys	Val	Lys	Asn	Phe	Glu	Gln
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Gly	Phe	Ile	Thr	Asp	Pro	Val	Val	Leu	Ser	Pro	Ser	His	Thr	Val	Gly
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Asp	Val	Leu	Glu	Ala	Lys	Met	Arg	His	Gly	Phe	Ser	Gly	Ile	Pro	Ile
	130					135					140				
Thr	Glu	Thr	Gly	Thr	Met	Gly	Ser	Lys	Leu	Val	Gly	Ile	Val	Thr	Ser
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Arg	Asp	Ile	Asp	Phe	Leu	Ala	Glu	Lys	Asp	His	Thr	Thr	Leu	Leu	Ser
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Glu	Val	Met	Thr	Pro	Arg	Ile	Glu	Leu	Val	Val	Ala	Pro	Ala	Gly	Val
			180					185					190		
Thr	Leu	Lys	Glu	Ala	Asn	Glu	Ile	Leu	Gln	Arg	Ser	Lys	Lys	Gly	Lys
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Leu	Pro	Ile	Val	Asn	Asp	Cys	Asp	Glu	Leu	Val	Ala	Ile	Ile	Ala	Arg
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Thr	Asp	Leu	Lys	Lys	Asn	Arg	Asp	Tyr	Pro	Leu	Ala	Ser	Lys	Asp	Ser
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Gln	Lys	Gln	Leu	Leu	Cys	Gly	Ala	Ala	Val	Gly	Thr	Arg	Glu	Asp	Asp
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Lys	Tyr	Arg	Leu	Asp	Leu	Leu	Thr	Gln	Ala	Gly	Val	Asp	Val	Ile	Val
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Phe	His	Ser	Ser	Gln	Gly	Asn	Ser	Val	Tyr	Gln	Ile	Ala	Met	Val	His
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Tyr	Ile	Lys	Gln	Lys	Tyr	Pro	His	Leu	Gln	Val	Ile	Gly	Gly	Asn	Val
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Val	Thr	Ala	Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	Asp	Gly
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Leu	Arg	Val	Gly	Met	Gly	Cys	Gly	Ser	Ile	Cys	Ile	Thr	Gln	Glu	Val
				325					330					335	
Met	Ala	Cys	Gly	Arg	Pro	Gln	Gly	Thr	Ala	Val	Tyr	Lys	Val	Ala	Glu
			340					345					350		
Tyr	Ala	Arg	Arg	Phe	Gly	Val	Pro	Ile	Ile	Ala	Asp	Gly	Gly	Ile	Gln
		355					360					365			
Thr	Val	Gly	His	Val	Val	Lys	Ala	Leu	Ala	Leu	Gly	Ala	Ser	Thr	Val
	370					375					380				
Met	Met	Gly	Ser	Leu	Leu	Ala	Ala	Thr	Thr	Glu	Ala	Pro	Gly	Glu	Tyr
385					390					395					400
Phe	Phe	Ser	Asp	Gly	Val	Arg	Leu	Lys	Lys	Tyr	Arg	Gly	Met	Gly	Ser
			405						410					415	
Leu	Asp	Pro	Met	Glu	Lys	Ser	Ser	Ser	Ser	Gln	Lys	Arg	Tyr	Phe	Ser
			420					425					430		
Glu	Gly	Asp	Lys	Val	Lys	Ile	Ala	Gln	Gly	Val	Ser	Gly	Ser	Ile	Gln
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Asp	Lys	Gly	Ser	Ile	Gln	Lys	Phe	Val	Pro	Tyr	Leu	Ile	Ala	Gly	Ile
	450					455					460				
Gln	His	Gly	Cys	Gln	Asp	Ile	Gly	Ala	Arg	Ser	Leu	Ser	Val	Leu	Arg
465					470					475					480
Ser	Met	Met	Tyr	Ser	Gly	Glu	Leu	Lys	Phe	Glu	Lys	Arg	Thr	Met	Ser
			485						490					495	
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 <223> Human wild-type Dihydroorotate Dehydrogenase  
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<300>  
 <301> Minet, M., Dufour, M-E., and Lacroute, F.  
 <302> Cloning and Sequencing of a Human cDNA coding for  
 <303> Gene (1992)  
 <304> 121  
 <306> 393-396

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 atc ctg ggg gga gga gga ctt ctc ttc gcc tcc tac ctg atg gcc acg 96  
 Ile Leu Gly Gly Gly Gly Leu Leu Phe Ala Ser Tyr Leu Met Ala Thr  
 20 25 30  
 gga gat gag cgt ttc tat gct gaa cac ctg atg ccg act ctg cag ggg 144  
 Gly Asp Glu Arg Phe Tyr Ala Glu His Leu Met Pro Thr Leu Gln Gly  
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 Leu Leu Asp Pro Glu Ser Ala His Arg Leu Ala Val Arg Phe Thr Ser  
 50 55 60  
 ctg ggg ctc ctt cca cgg gcc aga ttt caa gac tct gac atg ctg gaa 240  
 Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp Met Leu Glu  
 65 70 75 80  
 gtg aga gtt ctg ggc cat aaa ttc cga aat cca gta gga att gct gca 288  
 Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly Ile Ala Ala  
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 gga ttt gac aag cat ggg gaa gcc gtg gac gga ctt tat aag atg ggc 336  
 Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr Lys Met Gly  
 100 105 110  
 ttt ggt ttt gtt gag ata gga agt gtg act cca aaa cct cag gaa gga 384  
 Phe Gly Phe Val Glu Ile Gly Ser Val Thr Pro Lys Pro Gln Glu Gly  
 115 120 125  
 aac cct aga ccc aga gtc ttc cgc ctc cct gag gac caa gct gtc att 432  
 Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln Ala Val Ile  
 130 135 140  
 aac agg tat gga ttt aac agt cac ggg ctt tca gtg gtg gaa cac agg 480  
 Asn Arg Tyr Gly Phe Asn Ser His Gly Leu Ser Val Val Glu His Arg  
 145 150 155 160  
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 Leu Arg Ala Arg Gln Gln Lys Gln Ala Lys Leu Thr Glu Asp Gly Leu  
 165 170 175  
 cct ctg ggg gtc aac ttg ggg aag aac aag acc tca gtg gac gcc gcg 576  
 Pro Leu Gly Val Asn Leu Gly Lys Asn Lys Thr Ser Val Asp Ala Ala  
 180 185 190  
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 Glu Asp Tyr Ala Glu Gly Val Arg Val Leu Gly Pro Leu Ala Asp Tyr

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Leu	Val	Val	Asn	Val	Ser	Ser	Pro	Asn	Thr	Ala	Gly	Leu	Arg	Ser	Leu	
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cag	gga	aag	gcc	gag	ctg	cgc	cgc	ctg	ctg	acc	aag	gtg	ctg	cag	gag	720
Gln	Gly	Lys	Ala	Glu	Leu	Arg	Arg	Leu	Leu	Thr	Lys	Val	Leu	Gln	Glu	
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agg	gat	ggc	ttg	cgg	aga	gtg	cac	agg	ccg	gca	gtc	ctg	gtg	aag	atc	768
Arg	Asp	Gly	Leu	Arg	Arg	Val	His	Arg	Pro	Ala	Val	Leu	Val	Lys	Ile	
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Ala	Pro	Asp	Leu	Thr	Ser	Gln	Asp	Lys	Glu	Asp	Ile	Ala	Ser	Val	Val	
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Lys	Glu	Leu	Gly	Ile	Asp	Gly	Leu	Ile	Val	Thr	Asn	Thr	Thr	Val	Ser	
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Ser	Gly	Lys	Pro	Leu	Arg	Asp	Leu	Ser	Thr	Gln	Thr	Ile	Arg	Glu	Met	
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tat	gca	ctc	acc	caa	ggc	cga	gtt	ccc	ata	att	ggg	gtt	ggt	ggt	gtg	1008
Tyr	Ala	Leu	Thr	Gln	Gly	Arg	Val	Pro	Ile	Ile	Gly	Val	Gly	Gly	Val	
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Ser	Ser	Gly	Gln	Asp	Ala	Leu	Glu	Lys	Ile	Arg	Ala	Gly	Ala	Ser	Leu	
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Val	Gln	Leu	Tyr	Thr	Ala	Leu	Thr	Phe	Trp	Gly	Pro	Pro	Val	Val	Gly	
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Lys	Val	Lys	Arg	Glu	Leu	Glu	Ala	Leu	Leu	Lys	Glu	Gln	Gly	Phe	Gly	
	370					375					380					
gga	gtc	aca	gat	gcc	att	gga	gca	gat	cat	cgg	agg	tgaggacagc				1198
Gly	Val	Thr	Asp	Ala	Ile	Gly	Ala	Asp	His	Arg	Arg					
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<400> 20

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 Leu Leu Asp Pro Glu Ser Ala His Arg Leu Ala Val Arg Phe Thr Ser  
 50 55 60  
 Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp Met Leu Glu  
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 Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly Ile Ala Ala  
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 Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr Lys Met Gly  
 100 105 110  
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 130 135 140  
 Asn Arg Tyr Gly Phe Asn Ser His Gly Leu Ser Val Val Glu His Arg  
 145 150 155 160  
 Leu Arg Ala Arg Gln Gln Lys Gln Ala Lys Leu Thr Glu Asp Gly Leu  
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 Pro Leu Gly Val Asn Leu Gly Lys Asn Lys Thr Ser Val Asp Ala Ala  
 180 185 190  
 Glu Asp Tyr Ala Glu Gly Val Arg Val Leu Gly Pro Leu Ala Asp Tyr  
 195 200 205  
 Leu Val Val Asn Val Ser Ser Pro Asn Thr Ala Gly Leu Arg Ser Leu  
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 Gln Gly Lys Ala Glu Leu Arg Arg Leu Leu Thr Lys Val Leu Gln Glu  
 225 230 235 240  
 Arg Asp Gly Leu Arg Arg Val His Arg Pro Ala Val Leu Val Lys Ile  
 245 250 255  
 Ala Pro Asp Leu Thr Ser Gln Asp Lys Glu Asp Ile Ala Ser Val Val  
 260 265 270  
 Lys Glu Leu Gly Ile Asp Gly Leu Ile Val Thr Asn Thr Thr Val Ser  
 275 280 285  
 Arg Pro Ala Gly Leu Gln Gly Ala Leu Arg Ser Glu Thr Gly Gly Leu  
 290 295 300  
 Ser Gly Lys Pro Leu Arg Asp Leu Ser Thr Gln Thr Ile Arg Glu Met  
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 Tyr Ala Leu Thr Gln Gly Arg Val Pro Ile Ile Gly Val Gly Gly Val  
 325 330 335  
 Ser Ser Gly Gln Asp Ala Leu Glu Lys Ile Arg Ala Gly Ala Ser Leu  
 340 345 350  
 Val Gln Leu Tyr Thr Ala Leu Thr Phe Trp Gly Pro Pro Val Val Gly  
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 <222> (1)...(1101)  
 <223> DHODH Truncated 39 kDa Construct

<300>

<301> Copeland, R.A., et al.  
 <302> Recombinant Human Dihydroorotate Dehydrogenase  
 <303> Arch. Biochem. Biophys. (1995)  
 <304> 323  
 <306> 79-86

<400> 21

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Leu Gln Gly Leu Leu Asp Pro Glu Ser Ala His Arg Leu Ala Val Arg	
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ttc acc tcc ctg ggg ctc ctt cca cgg gcc aga ttt caa gac tct gac	144
Phe Thr Ser Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp	
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att gct gca gga ttt gac aag cat ggg gaa gcc gtg gac gga ctt tat	240
Ile Ala Ala Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr	
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Lys Met Gly Phe Gly Phe Val Glu Ile Gly Ser Val Thr Pro Lys Pro	
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Gln Glu Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln	
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gct gtc att aac agg tat gga ttt aac agt cac ggg ctt tca gtg gtg	384
Ala Val Ile Asn Arg Tyr Gly Phe Asn Ser His Gly Leu Ser Val Val	
115 120 125	
gaa cac agg tta cgg gcc aga cag cag aag cag gcc aag ctc aca gaa	432
Glu His Arg Leu Arg Ala Arg Gln Gln Lys Gln Ala Lys Leu Thr Glu	
130 135 140	
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Asp Gly Leu Pro Leu Gly Val Asn Leu Gly Lys Asn Lys Thr Ser Val	
145 150 155 160	
gac gcc gcg gag gac tac gca gaa ggg gtg cgc gta ctg ggc ccc ctg	528
Asp Ala Ala Glu Asp Tyr Ala Glu Gly Val Arg Val Leu Gly Pro Leu	
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gcc gac tac ctg gtg gtg aat gtg tcc agc ccc aac act gcc ggg ctg	576
Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Ala Gly Leu	
180 185 190	
cgg agc ctt cag gga aag gcc gag ctg cgc cgc ctg ctg acc aag gtg	624
Arg Ser Leu Gln Gly Lys Ala Glu Leu Arg Arg Leu Leu Thr Lys Val	
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ctg cag gag agg gat ggc ttg cgg aga gtg cac agg ccg gca gtc ctg	672
Leu Gln Glu Arg Asp Gly Leu Arg Arg Val His Arg Pro Ala Val Leu	
210 215 220	

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Ser	Val	Val	Lys	Glu	Leu	Gly	Ile	Asp	Gly	Leu	Ile	Val	Thr	Asn	Thr	
				245					250					255		
acc	gtg	agt	cgc	cct	gcg	ggc	ctc	cag	ggt	gcc	ctg	cgc	tct	gaa	aca	816
Thr	Val	Ser	Arg	Pro	Ala	Gly	Leu	Gln	Gly	Ala	Leu	Arg	Ser	Glu	Thr	
			260					265					270			
gga	ggg	ctg	agt	ggg	aag	ccc	ctc	cgg	gat	tta	tca	act	caa	acc	att	864
Gly	Gly	Leu	Ser	Gly	Lys	Pro	Leu	Arg	Asp	Leu	Ser	Thr	Gln	Thr	Ile	
		275					280					285				
cgg	gag	atg	tat	gca	ctc	acc	caa	ggc	cga	gtt	ccc	ata	att	ggg	gtt	912
Arg	Glu	Met	Tyr	Ala	Leu	Thr	Gln	Gly	Arg	Val	Pro	Ile	Ile	Gly	Val	
	290					295					300					
ggt	ggt	gtg	agc	agc	ggg	cag	gac	gcg	ctg	gag	aag	atc	cgg	gca	ggg	960
Gly	Gly	Val	Ser	Ser	Gly	Gln	Asp	Ala	Leu	Glu	Lys	Ile	Arg	Ala	Gly	
305					310					315					320	
gcc	tcc	ctg	gtg	cag	ctg	tac	acg	gcc	ctc	acc	ttc	tgg	ggg	cca	ccc	1008
Ala	Ser	Leu	Val	Gln	Leu	Tyr	Thr	Ala	Leu	Thr	Phe	Trp	Gly	Pro	Pro	
				325					330					335		
gtt	gtg	ggc	aaa	gtc	aag	cgg	gaa	ctg	gag	gcc	ctt	ctg	aaa	gag	cag	1056
Val	Val	Gly	Lys	Val	Lys	Arg	Glu	Leu	Glu	Ala	Leu	Leu	Lys	Glu	Gln	
			340					345					350			
ggc	ttt	ggc	gga	gtc	aca	gat	gcc	att	gga	gca	gat	cat	cgg	agg		1101
Gly	Phe	Gly	Gly	Val	Thr	Asp	Ala	Ile	Gly	Ala	Asp	His	Arg	Arg		
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<210> 22  
 <211> 367  
 <212> PRT  
 <213> Homo sapien

<400> 22  
 Met Ala Thr Gly Asp Glu Arg Phe Tyr Ala Glu His Leu Met Pro Thr  
 1 5 10 15  
 Leu Gln Gly Leu Leu Asp Pro Glu Ser Ala His Arg Leu Ala Val Arg  
 20 25 30  
 Phe Thr Ser Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp  
 35 40 45  
 Met Leu Glu Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly  
 50 55 60  
 Ile Ala Ala Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr  
 65 70 75 80  
 Lys Met Gly Phe Gly Phe Val Glu Ile Gly Ser Val Thr Pro Lys Pro  
 85 90 95  
 Gln Glu Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln  
 100 105 110  
 Ala Val Ile Asn Arg Tyr Gly Phe Asn Ser His Gly Leu Ser Val Val  
 115 120 125  
 Glu His Arg Leu Arg Ala Arg Gln Gln Lys Gln Ala Lys Leu Thr Glu  
 130 135 140



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Asp Gly Leu Pro Leu Gly Val Asn Leu Gly Lys Asn Lys Thr Ser Val
145      150      155      160
Asp Ala Ala Glu Asp Tyr Ala Glu Gly Val Arg Val Leu Gly Pro Leu
      165      170      175
Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Ala Gly Leu
      180      185      190
Arg Ser Leu Gln Gly Lys Ala Glu Leu Arg Arg Leu Leu Thr Lys Val
      195      200      205
Leu Gln Glu Arg Asp Gly Leu Arg Arg Val His Arg Pro Ala Val Leu
      210      215      220
Val Lys Ile Ala Pro Asp Leu Thr Ser Gln Asp Lys Glu Asp Ile Ala
225      230      235      240
Ser Val Val Lys Glu Leu Gly Ile Asp Gly Leu Ile Val Thr Asn Thr
      245      250      255
Thr Val Ser Arg Pro Ala Gly Leu Gln Gly Ala Leu Arg Ser Glu Thr
      260      265      270
Gly Gly Leu Ser Gly Lys Pro Leu Arg Asp Leu Ser Thr Gln Thr Ile
      275      280      285
Arg Glu Met Tyr Ala Leu Thr Gln Gly Arg Val Pro Ile Ile Gly Val
      290      295      300
Gly Gly Val Ser Ser Gly Gln Asp Ala Leu Glu Lys Ile Arg Ala Gly
305      310      315      320
Ala Ser Leu Val Gln Leu Tyr Thr Ala Leu Thr Phe Trp Gly Pro Pro
      325      330      335
Val Val Gly Lys Val Lys Arg Glu Leu Glu Ala Leu Leu Lys Glu Gln
      340      345      350
Gly Phe Gly Gly Val Thr Asp Ala Ile Gly Ala Asp His Arg Arg
      355      360      365

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<210> 23
<211> 1101
<212> DNA
<213> Homo sapien

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<220>
<221> mutation
<222> 79
<223> C to G mutation

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<221> mutation
<222> 80
<223> A to C mutation

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<221> CDS
<222> (4)...(1101)
<223> His26Ala DHODH mutant

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<300>
<301> Davis et al.
<302> Histidine to Alanine mutants of Human Dihydroorota
<303> Biochem. Pharmacol. (1997)
<304> 54
<306> 459-465

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<400> 23
atg gcc acg gga gat gag cgt ttc tat gct gaa cac ctg atg ccg act      48
  Ala Thr Gly Asp Glu Arg Phe Tyr Ala Glu His Leu Met Pro Thr
      1          5          10          15

ctg cag ggg ctg ctg gac ccg gag tca gcc gcc aga ctg gct gtt cgc      96
Leu Gln Gly Leu Leu Asp Pro Glu Ser Ala Ala Arg Leu Ala Val Arg
      20          25          30

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ttc	acc	tcc	ctg	ggg	ctc	ctt	cca	cgg	gcc	aga	ttt	caa	gac	tct	gac	144
Phe	Thr	Ser	Leu	Gly	Leu	Leu	Pro	Arg	Ala	Arg	Phe	Gln	Asp	Ser	Asp	
			35					40					45			
atg	ctg	gaa	gtg	aga	gtt	ctg	ggc	cat	aaa	ttc	cga	aat	cca	gta	gga	192
Met	Leu	Glu	Val	Arg	Val	Leu	Gly	His	Lys	Phe	Arg	Asn	Pro	Val	Gly	
		50					55					60				
att	gct	gca	gga	ttt	gac	aag	cat	ggg	gaa	gcc	gtg	gac	gga	ctt	tat	240
Ile	Ala	Ala	Gly	Phe	Asp	Lys	His	Gly	Glu	Ala	Val	Asp	Gly	Leu	Tyr	
	65					70					75					
aag	atg	ggc	ttt	ggt	ttt	gtt	gag	ata	gga	agt	gtg	act	cca	aaa	cct	288
Lys	Met	Gly	Phe	Gly	Phe	Val	Glu	Ile	Gly	Ser	Val	Thr	Pro	Lys	Pro	
80					85					90					95	
cag	gaa	gga	aac	cct	aga	ccc	aga	gtc	ttc	cgc	ctc	cct	gag	gac	caa	336
Gln	Glu	Gly	Asn	Pro	Arg	Pro	Arg	Val	Phe	Arg	Leu	Pro	Glu	Asp	Gln	
				100					105					110		
gct	gtc	att	aac	agg	tat	gga	ttt	aac	agt	cac	ggg	ctt	tca	gtg	gtg	384
Ala	Val	Ile	Asn	Arg	Tyr	Gly	Phe	Asn	Ser	His	Gly	Leu	Ser	Val	Val	
			115					120					125			
gaa	cac	agg	tta	cgg	gcc	aga	cag	cag	aag	cag	gcc	aag	ctc	aca	gaa	432
Glu	His	Arg	Leu	Arg	Ala	Arg	Gln	Gln	Lys	Gln	Ala	Lys	Leu	Thr	Glu	
		130					135					140				
gat	gga	ctg	cct	ctg	ggg	gtc	aac	ttg	ggg	aag	aac	aag	acc	tca	gtg	480
Asp	Gly	Leu	Pro	Leu	Gly	Val	Asn	Leu	Gly	Lys	Asn	Lys	Thr	Ser	Val	
	145					150					155					
gac	gcc	gcg	gag	gac	tac	gca	gaa	ggg	gtg	cgc	gta	ctg	ggc	ccc	ctg	528
Asp	Ala	Ala	Glu	Asp	Tyr	Ala	Glu	Gly	Val	Arg	Val	Leu	Gly	Pro	Leu	
160					165					170					175	
gcc	gac	tac	ctg	gtg	gtg	aat	gtg	tcc	agc	ccc	aac	act	gcc	ggg	ctg	576
Ala	Asp	Tyr	Leu	Val	Val	Asn	Val	Ser	Ser	Pro	Asn	Thr	Ala	Gly	Leu	
				180					185					190		
cgg	agc	ctt	cag	gga	aag	gcc	gag	ctg	cgc	cgc	ctg	ctg	acc	aag	gtg	624
Arg	Ser	Leu	Gln	Gly	Lys	Ala	Glu	Leu	Arg	Arg	Leu	Leu	Thr	Lys	Val	
			195					200					205			
ctg	cag	gag	agg	gat	ggc	ttg	cgg	aga	gtg	cac	agg	ccg	gca	gtc	ctg	672
Leu	Gln	Glu	Arg	Asp	Gly	Leu	Arg	Arg	Val	His	Arg	Pro	Ala	Val	Leu	
		210					215					220				
gtg	aag	atc	gct	cct	gac	ctc	acc	agc	cag	gat	aag	gag	gac	att	gcc	720
Val	Lys	Ile	Ala	Pro	Asp	Leu	Thr	Ser	Gln	Asp	Lys	Glu	Asp	Ile	Ala	
	225					230					235					
agt	gtg	gtc	aaa	gag	ttg	ggc	atc	gat	ggg	ctg	att	gtt	acg	aac	acc	768
Ser	Val	Val	Lys	Glu	Leu	Gly	Ile	Asp	Gly	Leu	Ile	Val	Thr	Asn	Thr	
240					245				250						255	
acc	gtg	agt	cgc	cct	gcg	ggc	ctc	cag	ggt	gcc	ctg	cgc	tct	gaa	aca	816
Thr	Val	Ser	Arg	Pro	Ala	Gly	Leu	Gln	Gly	Ala	Leu	Arg	Ser	Glu	Thr	
				260					265					270		
gga	ggg	ctg	agt	ggg	aag	ccc	ctc	cgg	gat	tta	tca	act	caa	acc	att	864

Gly	Gly	Leu	Ser	Gly	Lys	Pro	Leu	Arg	Asp	Leu	Ser	Thr	Gln	Thr	Ile	
			275					280					285			
cgg	gag	atg	tat	gca	ctc	acc	caa	ggc	cga	gtt	ccc	ata	att	ggg	gtt	912
Arg	Glu	Met	Tyr	Ala	Leu	Thr	Gln	Gly	Arg	Val	Pro	Ile	Ile	Gly	Val	
		290					295					300				
ggg	ggg	gtg	agc	agc	ggg	cag	gac	gcg	ctg	gag	aag	atc	cgg	gca	ggg	960
Gly	Gly	Val	Ser	Ser	Gly	Gln	Asp	Ala	Leu	Glu	Lys	Ile	Arg	Ala	Gly	
	305					310					315					
gcc	tcc	ctg	gtg	cag	ctg	tac	acg	gcc	ctc	acc	ttc	tgg	ggg	cca	ccc	1008
Ala	Ser	Leu	Val	Gln	Leu	Tyr	Thr	Ala	Leu	Thr	Phe	Trp	Gly	Pro	Pro	
320					325					330					335	
gtt	gtg	ggc	aaa	gtc	aag	cgg	gaa	ctg	gag	gcc	ctt	ctg	aaa	gag	cag	1056
Val	Val	Gly	Lys	Val	Lys	Arg	Glu	Leu	Glu	Ala	Leu	Leu	Lys	Glu	Gln	
				340				345						350		
ggc	ttt	ggc	gga	gtc	aca	gat	gcc	att	gga	gca	gat	cat	cgg	agg		1101
Gly	Phe	Gly	Gly	Val	Thr	Asp	Ala	Ile	Gly	Ala	Asp	His	Arg	Arg		
			355					360					365			

<210> 24  
 <211> 366  
 <212> PRT  
 <213> Homo sapien

<400> 24

Ala	Thr	Gly	Asp	Glu	Arg	Phe	Tyr	Ala	Glu	His	Leu	Met	Pro	Thr	Leu	
1				5					10					15		
Gln	Gly	Leu	Leu	Asp	Pro	Glu	Ser	Ala	Ala	Arg	Leu	Ala	Val	Arg	Phe	
		20						25					30			
Thr	Ser	Leu	Gly	Leu	Leu	Pro	Arg	Ala	Arg	Phe	Gln	Asp	Ser	Asp	Met	
		35					40					45				
Leu	Glu	Val	Arg	Val	Leu	Gly	His	Lys	Phe	Arg	Asn	Pro	Val	Gly	Ile	
	50					55					60					
Ala	Ala	Gly	Phe	Asp	Lys	His	Gly	Glu	Ala	Val	Asp	Gly	Leu	Tyr	Lys	
65				70						75					80	
Met	Gly	Phe	Gly	Phe	Val	Glu	Ile	Gly	Ser	Val	Thr	Pro	Lys	Pro	Gln	
			85					90						95		
Glu	Gly	Asn	Pro	Arg	Pro	Arg	Val	Phe	Arg	Leu	Pro	Glu	Asp	Gln	Ala	
		100						105					110			
Val	Ile	Asn	Arg	Tyr	Gly	Phe	Asn	Ser	His	Gly	Leu	Ser	Val	Val	Glu	
		115					120					125				
His	Arg	Leu	Arg	Ala	Arg	Gln	Gln	Lys	Gln	Ala	Lys	Leu	Thr	Glu	Asp	
	130					135					140					
Gly	Leu	Pro	Leu	Gly	Val	Asn	Leu	Gly	Lys	Asn	Lys	Thr	Ser	Val	Asp	
145				150						155					160	
Ala	Ala	Glu	Asp	Tyr	Ala	Glu	Gly	Val	Arg	Val	Leu	Gly	Pro	Leu	Ala	
			165					170						175		
Asp	Tyr	Leu	Val	Val	Asn	Val	Ser	Ser	Pro	Asn	Thr	Ala	Gly	Leu	Arg	
		180					185						190			
Ser	Leu	Gln	Gly	Lys	Ala	Glu	Leu	Arg	Arg	Leu	Leu	Thr	Lys	Val	Leu	
	195					200						205				
Gln	Glu	Arg	Asp	Gly	Leu	Arg	Arg	Val	His	Arg	Pro	Ala	Val	Leu	Val	
	210				215						220					
Lys	Ile	Ala	Pro	Asp	Leu	Thr	Ser	Gln	Asp	Lys	Glu	Asp	Ile	Ala	Ser	
225				230						235					240	
Val	Val	Lys	Glu	Leu	Gly	Ile	Asp	Gly	Leu	Ile	Val	Thr	Asn	Thr	Thr	
				245					250					255		

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Val Ser Arg Pro Ala Gly Leu Gln Gly Ala Leu Arg Ser Glu Thr Gly
      260      265      270
Gly Leu Ser Gly Lys Pro Leu Arg Asp Leu Ser Thr Gln Thr Ile Arg
      275      280      285
Glu Met Tyr Ala Leu Thr Gln Gly Arg Val Pro Ile Ile Gly Val Gly
      290      295      300
Gly Val Ser Ser Gly Gln Asp Ala Leu Glu Lys Ile Arg Ala Gly Ala
      305      310      315      320
Ser Leu Val Gln Leu Tyr Thr Ala Leu Thr Phe Trp Gly Pro Pro Val
      325      330      335
Val Gly Lys Val Lys Arg Glu Leu Glu Ala Leu Leu Lys Glu Gln Gly
      340      345      350
Phe Gly Gly Val Thr Asp Ala Ile Gly Ala Asp His Arg Arg
      355      360      365

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<210> 25
<211> 1560
<212> DNA
<213> Aspergillus nidulans

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<220>
<221> CDS
<222> (1)...(1560)
<223> Aspergillus nidulans Val200Glu mutant DHODH cDNA

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<221> mutation
<222> 599
<223> T to A mutataction

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<400> 25
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Met Ala Thr Asn Ser Phe Arg Lys Leu Thr Phe Ser Gly Ala Ser Arg
  1              5              10              15

ctg ggt ggt tgt cgc cgt ctc cca cta acc tgc aga caa ctt cga ttc      96
Leu Gly Gly Cys Arg Arg Leu Pro Leu Thr Cys Arg Gln Leu Arg Phe
              20              25              30

gcc tcc gac agc gga gcc gca gcg gca act aca aaa gca acg gcc gaa      144
Ala Ser Asp Ser Gly Ala Ala Ala Ala Thr Thr Lys Ala Thr Ala Glu
              35              40              45

tca gca gcc gag tca gct agt ata aac gtc aaa gag gca ccc aaa aag      192
Ser Ala Ala Glu Ser Ala Ser Ile Asn Val Lys Glu Ala Pro Lys Lys
              50              55              60

gcc gga cgg ggc ctg cgg cgc acg gtc ctg gga acg tcg ttg gcg ctg      240
Ala Gly Arg Gly Leu Arg Arg Thr Val Leu Gly Thr Ser Leu Ala Leu
      65              70              75              80

acg ctg ctg gtt gga tat gtc tac ggg acg gac acc cgg gcg agt gtg      288
Thr Leu Leu Val Gly Tyr Val Tyr Gly Thr Asp Thr Arg Ala Ser Val
              85              90              95

cat cgg tac ggt gtt gtg ccg ctg att aga gca ttg tat cct gat gcg      336
His Arg Tyr Gly Val Val Pro Leu Ile Arg Ala Leu Tyr Pro Asp Ala
              100              105              110

gaa gat gcg cat cat att ggt gtc gat act tta aag atg ctg tat aag      384
Glu Asp Ala His His Ile Gly Val Asp Thr Leu Lys Met Leu Tyr Lys
              115              120              125

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tat Tyr	ggt Gly	ctg Leu	cat His	cca Pro	agg Arg	gaa Glu	cgg Arg	ggg Gly	gat Asp	ccg Pro	gat Asp	gga Gly	gat Asp	ggg Gly	gcg Ala	432
	130					135				140						
ctg Leu	gcg Ala	aca Thr	gag Glu	gtc Val	ttt Phe	ggg Gly	tat Tyr	aca Thr	ctg Leu	tca Ser	aac Asn	cca Pro	att Ile	ggc Gly	ata Ile	480
	145				150					155					160	
tcg Ser	ggc Gly	ggc Gly	ctg Leu	gac Asp	aag Lys	cat His	gct Ala	gag Glu	atc Ile	cct Pro	gat Asp	ccg Pro	ctg Leu	ttc Phe	gcg Ala	528
				165					170					175		
atc Ile	ggt Gly	cct Pro	gcc Ala	att Ile	gtc Val	gaa Glu	gtc Val	ggg Gly	ggt Gly	acg Thr	aca Thr	ccc Pro	tta Leu	cca Pro	cag Gln	576
			180					185					190			
gat Asp	ggt Gly	aac Asn	ccg Pro	cgt Arg	cct Pro	cgc Arg	gaa Glu	ttc Phe	cga Arg	ctt Leu	cca Pro	tca Ser	cag Gln	aga Arg	gcg Ala	624
		195					200					205				
atg Met	ata Ile	aac Asn	cgg Arg	tac Tyr	ggc Gly	ctc Leu	aac Asn	tcc Ser	aaa Lys	ggc Gly	gca Ala	gat Asp	cac His	atg Met	gca Ala	672
	210					215					220					
gct Ala	atc Ile	ttg Leu	gag Glu	caa Gln	cga Arg	gta Val	cgc Arg	gat Asp	ttt Phe	gcc Ala	tac Tyr	gca Ala	aac Asn	gga Gly	ttt Phe	720
	225				230					235					240	
ggg Gly	gca Ala	tac Tyr	gat Asp	gcg Ala	gct Ala	aag Lys	cag Gln	cgt Arg	gta Val	ttg Leu	gac Asp	ggc Gly	gaa Glu	gct Ala	ggt Gly	768
				245					250					255		
gtg Val	cca Pro	cca Pro	ggt Gly	agt Ser	ctt Leu	cag Gln	cct Pro	ggt Gly	aag Lys	ctt Leu	tta Leu	gct Ala	gtc Val	caa Gln	gtg Val	816
			260					265					270			
gca Ala	aag Lys	aac Asn	aag Lys	gcc Ala	act Thr	cct Pro	gac Asp	ggc Gly	gac Asp	att Ile	gaa Glu	gcc Ala	atc Ile	aag Lys	cgc Arg	864
		275					280					285				
gac Asp	tat Tyr	gtg Val	tat Tyr	tgc Cys	gtg Val	gac Asp	cgt Arg	gtg Val	gcc Ala	aaa Lys	tac Tyr	gct Ala	gat Asp	att Ile	ctt Leu	912
	290					295					300					
gtt Val	gtg Val	aat Asn	gta Val	tcg Ser	agc Ser	ccc Pro	aac Asn	aca Thr	ccc Pro	ggt Gly	ctc Leu	cgt Arg	gac Asp	ctt Leu	caa Gln	960
	305				310					315					320	
gcc Ala	act Thr	gcc Ala	ccg Pro	ctc Leu	aca Thr	gct Ala	atc Ile	ttg Leu	agt Ser	gct Ala	gtc Val	gtt Val	ggc Gly	gcg Ala	gca Ala	1008
				325				330						335		
aag Lys	agc Ser	gtg Val	aac Asn	cgc Arg	aag Lys	acc Thr	aaa Lys	cca Pro	tat Tyr	gtt Val	atg Met	gtc Val	aag Lys	gtc Val	agt Ser	1056
			340					345					350			
ccg Pro	gat Asp	gaa Glu	gac Asp	tca Ser	gat Asp	gaa Glu	caa Gln	gtc Val	tct Ser	ggt Gly	atc Ile	tgc Cys	gac Asp	gcc Ala	gtc Val	1104
		355					360					365				
cga Arg	gca Ala	tcc Ser	ggt Gly	gtc Val	gac Asp	gga Gly	gtg Val	att Ile	gtc Val	gga Gly	aac Asn	aca Thr	aca Thr	aac Asn	cgt Arg	1152

370	375	380	
cgc ccc gac cct ata ccc caa ggt tac act ctt ccg gcc aag gag cag Arg Pro Asp Pro Ile Pro Gln Gly Tyr Thr Leu Pro Ala Lys Glu Gln 385 390 395 400			1200
gca acg ttg aaa gaa acc ggc ggg tat tca ggt cca cag ctg ttc gat Ala Thr Leu Lys Glu Thr Gly Gly Tyr Ser Gly Pro Gln Leu Phe Asp 405 410 415			1248
cgc aca gtg gcc ctt gtg gct cgg tac cgc tcc atg ctg gat gcg gag Arg Thr Val Ala Leu Val Ala Arg Tyr Arg Ser Met Leu Asp Ala Glu 420 425 430			1296
tcg gaa acg gcc gga tcc gcc aag gat tca gca gcg acc ata gcg caa Ser Glu Thr Ala Gly Ser Ala Lys Asp Ser Ala Ala Thr Ile Ala Gln 435 440 445			1344
aca gag cca ggc tcg gaa aac gtt cct cct gtg gaa gcg cca agc gga Thr Glu Pro Gly Ser Glu Asn Val Pro Pro Val Glu Ala Pro Ser Gly 450 455 460			1392
ctg ccg cgc aaa gtt atc ttc gct tcg ggt ggt atc acc aac ggg aag Leu Pro Arg Lys Val Ile Phe Ala Ser Gly Gly Ile Thr Asn Gly Lys 465 470 475 480			1440
cag gct cac gct gtt tta gac aca ggg gca tct gtt gcc atg atg tac Gln Ala His Ala Val Leu Asp Thr Gly Ala Ser Val Ala Met Met Tyr 485 490 495			1488
acc ggt gtg gtc tat ggt ggc gtc ggc act gtc act cga gtg aag caa Thr Gly Val Val Tyr Gly Gly Val Gly Thr Val Thr Arg Val Lys Gln 500 505 510			1536
gaa ctt cga acg gcg aaa aag gag Glu Leu Arg Thr Ala Lys Lys Glu 515 520			1560

<210> 26  
 <211> 520  
 <212> PRT  
 <213> Aspergillus nidulans

<400> 26  
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 Leu Gly Gly Cys Arg Arg Leu Pro Leu Thr Cys Arg Gln Leu Arg Phe  
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 Ala Ser Asp Ser Gly Ala Ala Ala Thr Thr Lys Ala Thr Ala Glu  
 35 40 45  
 Ser Ala Ala Glu Ser Ala Ser Ile Asn Val Lys Glu Ala Pro Lys Lys  
 50 55 60  
 Ala Gly Arg Gly Leu Arg Arg Thr Val Leu Gly Thr Ser Leu Ala Leu  
 65 70 75 80  
 Thr Leu Leu Val Gly Tyr Val Tyr Gly Thr Asp Thr Arg Ala Ser Val  
 85 90 95  
 His Arg Tyr Gly Val Val Pro Leu Ile Arg Ala Leu Tyr Pro Asp Ala  
 100 105 110  
 Glu Asp Ala His His Ile Gly Val Asp Thr Leu Lys Met Leu Tyr Lys  
 115 120 125  
 Tyr Gly Leu His Pro Arg Glu Arg Gly Asp Pro Asp Gly Asp Gly Ala

130	Leu	Ala	Thr	Glu	Val	Phe	135	Gly	Tyr	Thr	Leu	Ser	140	Asn	Pro	Ile	Gly	Ile
145	Ser	Gly	Gly	Leu	Asp	Lys	150	His	Ala	Glu	Ile	155	Pro	Asp	Pro	Leu	Phe	160
							165	Val	Glu	Val	Gly	170	Thr	Thr	Pro	Leu	Pro	175
	Ile	Gly	Pro	Ala	Ile	Val	180	Arg	Glu	Phe	Arg	185	Leu	Pro	Ser	Gln	Arg	190
	Asp	Gly	Asn	Pro	Arg	Pro	195	Gly	Leu	Asn	Ser	200	Gly	Ala	Asp	His	Met	205
	Met	Ile	Asn	Arg	Tyr	Gly	210	Val	Arg	Asp	Phe	215	Ala	Tyr	Ala	Asn	Gly	220
	Ala	Ile	Leu	Glu	Gln	Arg	225	Ala	Lys	Gln	Arg	230	Val	Leu	Asp	Gly	Glu	235
	Gly	Ala	Tyr	Asp	Ala	Ala	245	Leu	Gln	Pro	Gly	250	Lys	Leu	Leu	Ala	Val	255
	Val	Pro	Pro	Gly	Ser	Leu	260	Gln	Pro	Gly	Lys	265	Leu	Leu	Ala	Val	Gln	270
	Ala	Lys	Asn	Lys	Ala	Thr	275	Pro	Asp	Gly	Asp	280	Ile	Glu	Ala	Ile	Lys	285
	Asp	Tyr	Val	Tyr	Cys	Val	290	Asp	Arg	Val	Ala	295	Lys	Tyr	Ala	Asp	Ile	300
	Val	Val	Asn	Val	Ser	Ser	305	Pro	Asn	Thr	Pro	310	Gly	Leu	Arg	Asp	Leu	315
	Ala	Thr	Ala	Pro	Leu	Thr	325	Ala	Ile	Leu	Ser	330	Ala	Val	Val	Gly	Ala	335
	Lys	Ser	Val	Asn	Arg	Lys	340	Thr	Lys	Pro	Tyr	345	Val	Met	Val	Lys	Val	350
	Pro	Asp	Glu	Asp	Ser	Asp	355	Gln	Val	Ser	Gly	360	Ile	Cys	Asp	Ala	Val	365
	Arg	Ala	Ser	Gly	Val	Asp	370	Gly	Val	Ile	Val	375	Gly	Asn	Thr	Thr	Asn	380
	Arg	Pro	Asp	Pro	Ile	Pro	385	Gln	Gly	Tyr	Thr	390	Leu	Pro	Ala	Lys	Glu	395
	Ala	Thr	Leu	Lys	Glu	Thr	405	Gly	Gly	Tyr	Ser	410	Gly	Pro	Gln	Leu	Phe	415
	Arg	Thr	Val	Ala	Leu	Val	420	Ala	Arg	Tyr	Arg	425	Ser	Met	Leu	Asp	Ala	430
	Ser	Glu	Thr	Ala	Gly	Ser	435	Ala	Lys	Asp	Ser	440	Ala	Ala	Thr	Ile	Ala	445
	Thr	Glu	Pro	Gly	Ser	Glu	450	Asn	Val	Pro	Pro	455	Val	Glu	Ala	Pro	Ser	460
	Leu	Pro	Arg	Lys	Val	Ile	465	Phe	Ala	Ser	Gly	470	Gly	Ile	Thr	Asn	Gly	475
	Gln	Ala	His	Ala	Val	Leu	485	Asp	Thr	Gly	Ala	490	Ser	Val	Ala	Met	Met	495
	Thr	Gly	Val	Val	Tyr	Gly	500	Gly	Gly	Val	Gly	505	Thr	Val	Thr	Arg	Val	510
	Glu	Leu	Arg	Thr	Ala	Lys	515	Lys	Glu			520						

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<221> mutation  
 <222> 344

&lt;223&gt; C to T mutation

&lt;400&gt; 27

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ctg ggt ggt tgt cgc cgt ctc cca cta acc tgc aga caa ctt cga ttc	96
Leu Gly Gly Cys Arg Arg Leu Pro Leu Thr Cys Arg Gln Leu Arg Phe	
20 25 30	
gcc tcc gac agc gga gcc gca gcg gca act aca aaa gca acg gcc gaa	144
Ala Ser Asp Ser Gly Ala Ala Ala Thr Thr Lys Ala Thr Ala Glu	
35 40 45	
tca gca gcc gag tca gct agt ata aac gtc aaa gag gca ccc aaa aag	192
Ser Ala Ala Glu Ser Ala Ser Ile Asn Val Lys Glu Ala Pro Lys Lys	
50 55 60	
gcc gga cgg ggc ctg cgg cgc acg gtc ctg gga acg tcg ttg gcg ctg	240
Ala Gly Arg Gly Leu Arg Arg Thr Val Leu Gly Thr Ser Leu Ala Leu	
65 70 75 80	
acg ctg ctg gtt gga tat gtc tac ggg acg gac acc cgg gcg agt gtg	288
Thr Leu Leu Val Gly Tyr Val Tyr Gly Thr Asp Thr Arg Ala Ser Val	
85 90 95	
cat cgg tac ggt gtt gtg ccg ctg att aga gca ttg tat cct gat gcg	336
His Arg Tyr Gly Val Val Pro Leu Ile Arg Ala Leu Tyr Pro Asp Ala	
100 105 110	
gaa gat gtg cat cat att ggt gtc gat act tta aag atg ctg tat aag	384
Glu Asp Val His His Ile Gly Val Asp Thr Leu Lys Met Leu Tyr Lys	
115 120 125	
tat ggt ctg cat cca agg gaa cgg ggg gat ccg gat gga gat ggg gcg	432
Tyr Gly Leu His Pro Arg Glu Arg Gly Asp Pro Asp Gly Asp Gly Ala	
130 135 140	
ctg gcg aca gag gtc ttt ggg tat aca ctg tca aac cca att ggc ata	480
Leu Ala Thr Glu Val Phe Gly Tyr Thr Leu Ser Asn Pro Ile Gly Ile	
145 150 155 160	
tcg ggc ggc ctg gac aag cat gct gag atc cct gat ccg ctg ttc gcg	528
Ser Gly Gly Leu Asp Lys His Ala Glu Ile Pro Asp Pro Leu Phe Ala	
165 170 175	
atc ggt cct gcc att gtc gaa gtc ggg ggt acg aca ccc tta cca cag	576
Ile Gly Pro Ala Ile Val Glu Val Gly Gly Thr Thr Pro Leu Pro Gln	
180 185 190	
gat ggt aac ccg cgt cct cgc gta ttc cga ctt cca tca cag aga gcg	624
Asp Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Ser Gln Arg Ala	
195 200 205	
atg ata aac cgg tac ggc ctc aac tcc aaa ggc gca gat cac atg gca	672
Met Ile Asn Arg Tyr Gly Leu Asn Ser Lys Gly Ala Asp His Met Ala	
210 215 220	
gct atc ttg gag caa cga gta cgc gat ttt gcc tac gca aac gga ttt	720
Ala Ile Leu Glu Gln Arg Val Arg Asp Phe Ala Tyr Ala Asn Gly Phe	
225 230 235 240	



ggg gca tac gat gcg gct aag cag cgt gta ttg gac ggc gaa gct ggt Gly Ala Tyr Asp Ala Ala Lys Gln Arg Val Leu Asp Gly Glu Ala Gly	768
gtg cca cca ggt agt ctt cag cct ggt aag ctt tta gct gtc caa gtg Val Pro Pro Gly Ser Leu Gln Pro Gly Lys Leu Leu Ala Val Gln Val	816
gca aag aac aag gcc act cct gac ggc gac att gaa gcc atc aag cgc Ala Lys Asn Lys Ala Thr Pro Asp Gly Asp Ile Glu Ala Ile Lys Arg	864
gac tat gtg tat tgc gtg gac cgt gtg gcc aaa tac gct gat att ctt Asp Tyr Val Tyr Cys Val Asp Arg Val Ala Lys Tyr Ala Asp Ile Leu	912
gtt gtg aat gta tcg agc ccc aac aca ccc ggt ctc cgt gac ctt caa Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly Leu Arg Asp Leu Gln	960
gcc act gcc ccg ctc aca gct atc ttg agt gct gtc gtt ggc gcg gca Ala Thr Ala Pro Leu Thr Ala Ile Leu Ser Ala Val Val Gly Ala Ala	1008
aag agc gtg aac cgc aag acc aaa cca tat gtt atg gtc aag gtc agt Lys Ser Val Asn Arg Lys Thr Lys Pro Tyr Val Met Val Lys Val Ser	1056
ccg gat gaa gac tca gat gaa caa gtc tct ggt atc tgc gac gcc gtc Pro Asp Glu Asp Ser Asp Glu Gln Val Ser Gly Ile Cys Asp Ala Val	1104
cga gca tcc ggt gtc gac gga gtg att gtc gga aac aca aca aac cgt Arg Ala Ser Gly Val Asp Gly Val Ile Val Gly Asn Thr Thr Asn Arg	1152
cgc ccc gac cct ata ccc caa ggt tac act ctt ccg gcc aag gag cag Arg Pro Asp Pro Ile Pro Gln Gly Tyr Thr Leu Pro Ala Lys Glu Gln	1200
gca acg ttg aaa gaa acc ggc ggg tat tca ggt cca cag ctg ttc gat Ala Thr Leu Lys Glu Thr Gly Gly Tyr Ser Gly Pro Gln Leu Phe Asp	1248
cgc aca gtg gcc ctt gtg gct cgg tac cgc tcc atg ctg gat gcg gag Arg Thr Val Ala Leu Val Ala Arg Tyr Arg Ser Met Leu Asp Ala Glu	1296
tcg gaa acg gcc gga tcc gcc aag gat tca gca gcg acc ata gcg caa Ser Glu Thr Ala Gly Ser Ala Lys Asp Ser Ala Ala Thr Ile Ala Gln	1344
aca gag cca ggc tcg gaa aac gtt cct cct gtg gaa gcg cca agc gga Thr Glu Pro Gly Ser Glu Asn Val Pro Pro Val Glu Ala Pro Ser Gly	1392
ctg ccg cgc aaa gtt atc ttc gct tcg ggt ggt atc acc aac ggg aag Leu Pro Arg Lys Val Ile Phe Ala Ser Gly Gly Ile Thr Asn Gly Lys	1440
cag gct cac gct gtt tta gac aca ggg gca tct gtt gcc atg atg tac	1488

Gln Ala His Ala Val Leu Asp Thr Gly Ala Ser Val Ala Met Met Tyr  
485 490 495

acc ggt gtg gtc tat ggt ggc gtc ggc act gtc act cga gtg aag caa 1536  
Thr Gly Val Val Tyr Gly Gly Val Gly Thr Val Thr Arg Val Lys Gln  
500 505 510

gaa ctt cga acg gcg aaa aag gag 1560  
Glu Leu Arg Thr Ala Lys Lys Glu  
515 520

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<212> PRT  
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Ala Ser Asp Ser Gly Ala Ala Ala Thr Thr Lys Ala Thr Ala Glu  
35 40 45  
Ser Ala Ala Glu Ser Ala Ser Ile Asn Val Lys Glu Ala Pro Lys Lys  
50 55 60  
Ala Gly Arg Gly Leu Arg Arg Thr Val Leu Gly Thr Ser Leu Ala Leu  
65 70 75 80  
Thr Leu Leu Val Gly Tyr Val Tyr Gly Thr Asp Thr Arg Ala Ser Val  
85 90 95  
His Arg Tyr Gly Val Val Pro Leu Ile Arg Ala Leu Tyr Pro Asp Ala  
100 105 110  
Glu Asp Val His His Ile Gly Val Asp Thr Leu Lys Met Leu Tyr Lys  
115 120 125  
Tyr Gly Leu His Pro Arg Glu Arg Gly Asp Pro Asp Gly Asp Gly Ala  
130 135 140  
Leu Ala Thr Glu Val Phe Gly Tyr Thr Leu Ser Asn Pro Ile Gly Ile  
145 150 155 160  
Ser Gly Gly Leu Asp Lys His Ala Glu Ile Pro Asp Pro Leu Phe Ala  
165 170 175  
Ile Gly Pro Ala Ile Val Glu Val Gly Gly Thr Thr Pro Leu Pro Gln  
180 185 190  
Asp Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Ser Gln Arg Ala  
195 200 205  
Met Ile Asn Arg Tyr Gly Leu Asn Ser Lys Gly Ala Asp His Met Ala  
210 215 220  
Ala Ile Leu Glu Gln Arg Val Arg Asp Phe Ala Tyr Ala Asn Gly Phe  
225 230 235 240  
Gly Ala Tyr Asp Ala Ala Lys Gln Arg Val Leu Asp Gly Glu Ala Gly  
245 250 255  
Val Pro Pro Gly Ser Leu Gln Pro Gly Lys Leu Leu Ala Val Gln Val  
260 265 270  
Ala Lys Asn Lys Ala Thr Pro Asp Gly Asp Ile Glu Ala Ile Lys Arg  
275 280 285  
Asp Tyr Val Tyr Cys Val Asp Arg Val Ala Lys Tyr Ala Asp Ile Leu  
290 295 300  
Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly Leu Arg Asp Leu Gln  
305 310 315 320  
Ala Thr Ala Pro Leu Thr Ala Ile Leu Ser Ala Val Val Gly Ala Ala  
325 330 335  
Lys Ser Val Asn Arg Lys Thr Lys Pro Tyr Val Met Val Lys Val Ser  
340 345 350

Pro Asp Glu Asp Ser Asp Glu Gln Val Ser Gly Ile Cys Asp Ala Val  
 355 360 365  
 Arg Ala Ser Gly Val Asp Gly Val Ile Val Gly Asn Thr Thr Asn Arg  
 370 375 380  
 Arg Pro Asp Pro Ile Pro Gln Gly Tyr Thr Leu Pro Ala Lys Glu Gln  
 385 390 395 400  
 Ala Thr Leu Lys Glu Thr Gly Gly Tyr Ser Gly Pro Gln Leu Phe Asp  
 405 410 415  
 Arg Thr Val Ala Leu Val Ala Arg Tyr Arg Ser Met Leu Asp Ala Glu  
 420 425 430  
 Ser Glu Thr Ala Gly Ser Ala Lys Asp Ser Ala Ala Thr Ile Ala Gln  
 435 440 445  
 Thr Glu Pro Gly Ser Glu Asn Val Pro Pro Val Glu Ala Pro Ser Gly  
 450 455 460  
 Leu Pro Arg Lys Val Ile Phe Ala Ser Gly Gly Ile Thr Asn Gly Lys  
 465 470 475 480  
 Gln Ala His Ala Val Leu Asp Thr Gly Ala Ser Val Ala Met Met Tyr  
 485 490 495  
 Thr Gly Val Val Tyr Gly Gly Val Gly Thr Val Thr Arg Val Lys Gln  
 500 505 510  
 Glu Leu Arg Thr Ala Lys Lys Glu  
 515 520

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&lt;211&gt; 1707

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (67)...(1611)

&lt;223&gt; wild-type IMP dehydrogenase cDNA

&lt;400&gt; 29

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 gtgggtc atg gcg gac tac ctg att agc gga ggc acc tct tac gtg ccg 108  
 Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro  
 1 5 10

gac gac ggg ctc aca gcg cag cag ctc ttc aac tgc ggg gac ggc ctc 156  
 Asp Asp Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu  
 15 20 25 30

acc tac aat gat ttt ctc att ctt cct ggg tat atc gac ttc act gca 204  
 Thr Tyr Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala  
 35 40 45

gat cag gtg gac ttg acg tct gct cta act aag aag att aca cta aag 252  
 Asp Gln Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys  
 50 55 60

acc cca ttg gtt tcc tca ccc atg gac act gtc aca gag gct gga atg 300  
 Thr Pro Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met  
 65 70 75

gcc atc gcg atg gcg ctt aca gga ggt att ggt ttc atc cac cac aac 348  
 Ala Ile Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn  
 80 85 90

tgc aca cct gaa ttc cag gcc aat gaa gtt cgg aaa gtg aag aaa tac 396  
 Cys Thr Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr  
 95 100 105 110

gaa	cag	gga	ttc	atc	act	gac	ccc	gtg	gtc	ctt	agc	ccc	aag	gat	cgt	444
Glu	Gln	Gly	Phe	Ile	Thr	Asp	Pro	Val	Val	Leu	Ser	Pro	Lys	Asp	Arg	
				115					120					125		
gta	cgc	gat	gtt	ttt	gag	gcc	aaa	gcc	agg	cat	ggc	ttc	tgt	ggg	atc	492
Val	Arg	Asp	Val	Phe	Glu	Ala	Lys	Ala	Arg	His	Gly	Phe	Cys	Gly	Ile	
			130					135					140			
ccc	atc	aca	gat	aca	ggc	cgg	atg	ggg	agt	cga	ttg	gtg	ggc	atc	atc	540
Pro	Ile	Thr	Asp	Thr	Gly	Arg	Met	Gly	Ser	Arg	Leu	Val	Gly	Ile	Ile	
		145					150					155				
tcc	tca	agg	gac	att	gat	ttc	ctc	aag	gag	gaa	gag	cat	gac	cgg	ttc	588
Ser	Ser	Arg	Asp	Ile	Asp	Phe	Leu	Lys	Glu	Glu	Glu	His	Asp	Arg	Phe	
	160					165					170					
ttg	gaa	gag	atc	atg	act	aag	agg	gaa	gat	ttg	gtg	gtc	gcc	cct	gcc	636
Leu	Glu	Glu	Ile	Met	Thr	Lys	Arg	Glu	Asp	Leu	Val	Val	Ala	Pro	Ala	
175					180					185					190	
ggc	gtc	act	ctg	aaa	gag	gca	aat	gag	att	ctg	cag	cga	agt	aaa	aag	684
Gly	Val	Thr	Leu	Lys	Glu	Ala	Asn	Glu	Ile	Leu	Gln	Arg	Ser	Lys	Lys	
			195						200					205		
gga	aag	ttg	ccc	att	gtg	aat	gaa	aat	gat	gag	ctg	gta	gcc	atc	att	732
Gly	Lys	Leu	Pro	Ile	Val	Asn	Glu	Asn	Asp	Glu	Leu	Val	Ala	Ile	Ile	
			210					215					220			
gcc	cgg	aca	gac	cta	aag	aag	aat	cgt	gat	tac	ccc	ctg	gcc	tcc	aaa	780
Ala	Arg	Thr	Asp	Leu	Lys	Lys	Asn	Arg	Asp	Tyr	Pro	Leu	Ala	Ser	Lys	
		225					230					235				
gat	gcc	aag	aag	caa	ctg	ctg	tgt	ggg	gca	gcc	att	ggc	act	cat	gag	828
Asp	Ala	Lys	Lys	Gln	Leu	Leu	Cys	Gly	Ala	Ala	Ile	Gly	Thr	His	Glu	
	240				245						250					
gat	gac	aag	tat	agg	ctg	gac	tta	ctg	gcc	ctt	gct	ggg	gtg	gat	gta	876
Asp	Asp	Lys	Tyr	Arg	Leu	Asp	Leu	Leu	Ala	Leu	Ala	Gly	Val	Asp	Val	
255					260					265					270	
gtg	gtt	ttg	gac	tct	tcc	cag	gga	aac	tcc	atc	ttc	caa	atc	aat	atg	924
Val	Val	Leu	Asp	Ser	Ser	Gln	Gly	Asn	Ser	Ile	Phe	Gln	Ile	Asn	Met	
				275					280					285		
atc	aaa	tac	atc	aag	gag	aag	tat	ccc	agt	cta	cag	gtc	att	gga	ggc	972
Ile	Lys	Tyr	Ile	Lys	Glu	Lys	Tyr	Pro	Ser	Leu	Gln	Val	Ile	Gly	Gly	
			290					295					300			
aat	gta	gtc	act	gct	gcg	caa	gcc	aag	aac	ctc	ata	gat	gca	ggg	gta	1020
Asn	Val	Val	Thr	Ala	Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	
		305					310					315				
gat	gct	ttg	cga	gtc	ggc	atg	gga	agt	ggg	tcc	atc	tgc	atc	acc	cag	1068
Asp	Ala	Leu	Arg	Val	Gly	Met	Gly	Ser	Gly	Ser	Ile	Cys	Ile	Thr	Gln	
	320					325					330					
gaa	gtg	ttg	gcc	tgt	ggg	cgg	ccc	caa	gcc	aca	gca	gtg	tac	aag	gtc	1116
Glu	Val	Leu	Ala	Cys	Gly	Arg	Pro	Gln	Ala	Thr	Ala	Val	Tyr	Lys	Val	
335					340					345					350	
tct	gag	tat	gcc	cgt	cgc	ttt	ggg	gtt	cct	gtt	att	gct	gat	gga	gga	1164

Ser Glu Tyr Ala Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly  
 355 360 365

atc caa aat gtg ggt cat att gcc aaa gct ttg gct ctt ggg gct tcc 1212  
 Ile Gln Asn Val Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser  
 370 375 380

aca gtc atg atg ggc tcc ctc ctg gct gcc acc act gag gcc cct ggc 1260  
 Thr Val Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly  
 385 390 395

gag tac ttc ttc tca gat ggg atc cgg ctg aag aaa tac cga ggt atg 1308  
 Glu Tyr Phe Phe Ser Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met  
 400 405 410

ggt tct ctt gat gcc atg gac aaa cat ctc agc agc cag aac cga tac 1356  
 Gly Ser Leu Asp Ala Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr  
 415 420 425 430

ttc agt gaa gct gac aaa atc aaa gtg gcc caa gga gtt tca ggg gca 1404  
 Phe Ser Glu Ala Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala  
 435 440 445

gtg cag gac aag ggg tct atc cac aag ttc gtt cct tac ctg att gct 1452  
 Val Gln Asp Lys Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala  
 450 455 460

ggc atc cag cat tcc tgt caa gac att ggt gcc aag agt tta acc caa 1500  
 Gly Ile Gln His Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln  
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gtc aga gcc atg acg tac tcg ggg gag ctt aaa ttt gag aag agg aca 1548  
 Val Arg Ala Met Thr Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr  
 480 485 490

tcc tct gct cag gtg gaa ggt ggc gtc cac agc ctc cat tcg tac gag 1596  
 Ser Ser Ala Gln Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu  
 495 500 505 510

aaa cgg ctt ttc tga aaacagatcc agtatatgcc ttgaattttt caataaaagt 1651  
 Lys Arg Leu Phe \*

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 Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln  
 35 40 45  
 Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro  
 50 55 60  
 Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile  
 65 70 75 80  
 Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr

				85				90					95			
Pro	Glu	Phe	Gln	Ala	Asn	Glu	Val	Arg	Lys	Val	Lys	Lys	Tyr	Glu	Gln	
			100					105					110			
Gly	Phe	Ile	Thr	Asp	Pro	Val	Val	Leu	Ser	Pro	Lys	Asp	Arg	Val	Arg	
		115					120					125				
Asp	Val	Phe	Glu	Ala	Lys	Ala	Arg	His	Gly	Phe	Cys	Gly	Ile	Pro	Ile	
	130					135					140					
Thr	Asp	Thr	Gly	Arg	Met	Gly	Ser	Arg	Leu	Val	Gly	Ile	Ile	Ser	Ser	
145					150					155					160	
Arg	Asp	Ile	Asp	Phe	Leu	Lys	Glu	Glu	Glu	His	Asp	Arg	Phe	Leu	Glu	
				165				170						175		
Glu	Ile	Met	Thr	Lys	Arg	Glu	Asp	Leu	Val	Val	Ala	Pro	Ala	Gly	Val	
			180					185					190			
Thr	Leu	Lys	Glu	Ala	Asn	Glu	Ile	Leu	Gln	Arg	Ser	Lys	Lys	Gly	Lys	
		195					200					205				
Leu	Pro	Ile	Val	Asn	Glu	Asn	Asp	Glu	Leu	Val	Ala	Ile	Ile	Ala	Arg	
	210					215					220					
Thr	Asp	Leu	Lys	Lys	Asn	Arg	Asp	Tyr	Pro	Leu	Ala	Ser	Lys	Asp	Ala	
225					230					235					240	
Lys	Lys	Gln	Leu	Leu	Cys	Gly	Ala	Ala	Ile	Gly	Thr	His	Glu	Asp	Asp	
				245				250						255		
Lys	Tyr	Arg	Leu	Asp	Leu	Leu	Ala	Leu	Ala	Gly	Val	Asp	Val	Val	Val	
			260					265					270			
Leu	Asp	Ser	Ser	Gln	Gly	Asn	Ser	Ile	Phe	Gln	Ile	Asn	Met	Ile	Lys	
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Tyr	Ile	Lys	Glu	Lys	Tyr	Pro	Ser	Leu	Gln	Val	Ile	Gly	Gly	Asn	Val	
	290					295					300					
Val	Thr	Ala	Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	Asp	Ala	
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Leu	Arg	Val	Gly	Met	Gly	Ser	Gly	Ser	Ile	Cys	Ile	Thr	Gln	Glu	Val	
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Leu	Ala	Cys	Gly	Arg	Pro	Gln	Ala	Thr	Ala	Val	Tyr	Lys	Val	Ser	Glu	
			340					345					350			
Tyr	Ala	Arg	Arg	Phe	Gly	Val	Pro	Val	Ile	Ala	Asp	Gly	Gly	Ile	Gln	
		355					360					365				
Asn	Val	Gly	His	Ile	Ala	Lys	Ala	Leu	Ala	Leu	Gly	Ala	Ser	Thr	Val	
	370					375					380					
Met	Met	Gly	Ser	Leu	Leu	Ala	Ala	Thr	Thr	Glu	Ala	Pro	Gly	Glu	Tyr	
385					390					395					400	
Phe	Phe	Ser	Asp	Gly	Ile	Arg	Leu	Lys	Lys	Tyr	Arg	Gly	Met	Gly	Ser	
				405					410					415		
Leu	Asp	Ala	Met	Asp	Lys	His	Leu	Ser	Ser	Gln	Asn	Arg	Tyr	Phe	Ser	
			420					425					430			
Glu	Ala	Asp	Lys	Ile	Lys	Val	Ala	Gln	Gly	Val	Ser	Gly	Ala	Val	Gln	
		435					440					445				
Asp	Lys	Gly	Ser	Ile	His	Lys	Phe	Val	Pro	Tyr	Leu	Ile	Ala	Gly	Ile	
	450					455					460					
Gln	His	Ser	Cys	Gln	Asp	Ile	Gly	Ala	Lys	Ser	Leu	Thr	Gln	Val	Arg	
465					470					475					480	
Ala	Met	Thr	Tyr	Ser	Gly	Glu	Leu	Lys	Phe	Glu	Lys	Arg	Thr	Ser	Ser	
				485				490						495		
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Leu	Phe															

<210> 31  
 <211> 1707  
 <212> DNA  
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<220>

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       Ser351Tyr

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 <223> C to T mutation

<221> mutation  
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 <223> C to A mutation

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       Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro  
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gac gac ggg ctc aca gcg cag cag ctc ttc aac tgc ggg gac ggc ctc 156  
 Asp Asp Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu  
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acc tac aat gat ttt ctc att ctt cct ggg tat atc gac ttc act gca 204  
 Thr Tyr Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala  
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gat cag gtg gac ttg acg tct gct cta act aag aag att aca cta aag 252  
 Asp Gln Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys  
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acc cca ttg gtt tcc tca ccc atg gac act gtc aca gag gct gga atg 300  
 Thr Pro Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met  
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gcc atc gcg atg gcg ctt aca gga ggt att ggt ttc atc cac cac aac 348  
 Ala Ile Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn  
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tgc aca cct gaa ttc cag gcc aat gaa gtt cgg aaa gtg aag aaa tac 396  
 Cys Thr Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr  
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gaa cag gga ttc atc act gac ccc gtg gtc ctt agc ccc aag gat cgt 444  
 Glu Gln Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg  
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gta cgc gat gtt ttt gag gcc aaa gcc agg cat ggc ttc tgt ggt atc 492  
 Val Arg Asp Val Phe Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile  
                   130                  135                  140

ccc atc aca gat aca ggc cgg atg ggg agt cga ttg gtg ggc atc atc 540  
 Pro Ile Thr Asp Thr Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile  
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tcc tca agg gac att gat ttc ctc aag gag gaa gag cat gac cgg ttc 588  
 Ser Ser Arg Asp Ile Asp Phe Leu Lys Glu Glu Glu His Asp Arg Phe  
       160                  165                  170

ttg gaa gag atc atg act aag agg gaa gat ttg gtg gtc gcc cct gcc 636  
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Gly Val Thr Leu Lys 195		Glu Ala Asn Glu Ile 200		Leu Gln Arg Ser Lys 205		Lys	
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Gly Lys Leu Pro 210		Val Asn Glu Asn Asp 215		Leu Val Ala Ile Ile 220			
gcc cgg aca gac cta aag aag aat cgt gat tac ccc ctg gcc tcc aaa							780
Ala Arg Thr 225		Leu Lys Lys Asn Arg Asp Tyr Pro 235		Leu Ala Ser Lys			
gat gcc aag aag caa ctg ctg tgt ggg gca gcc att ggc act cat gag							828
Asp Ala Lys Lys Gln Leu 245		Cys Gly Ala Ala 250		Ile Gly Thr His Glu			
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Asp Asp Lys Tyr Arg 260		Leu Asp Leu Leu Ala 265		Ala Gly Val Asp Val 270			
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Val Val Leu Asp Ser 275		Gln Gly Asn Ser Ile Phe Gln Ile Asn Met 285					
atc aaa tac atc aag gag aag tat ccc agt cta cag gtc att gga ggc							972
Ile Lys Tyr Ile Lys Glu Lys Tyr 295		Pro Ser Leu Gln Val 300		Ile Gly Gly			
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Asn Val Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val 305		310		315			
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Asp Ala Leu Arg Val Gly Met 325		Gly Ser Gly Ser Ile Cys Ile Ile Gln 330					
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Glu Val Leu Ala Cys Gly Arg Pro Gln Ala Thr 345		Ala Val Tyr Lys Val 350					
tat gag tat gcc cgt cgc ttt ggt gtt cct gtt att gct gat gga gga							1164
Tyr Glu Tyr Ala Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly 355		360		365			
atc caa aat gtg ggt cat att gcc aaa gct ttg gct ctt ggg gct tcc							1212
Ile Gln Asn Val Gly His Ile Ala Lys 375		Ala Leu Ala Leu Gly Ala Ser 380					
aca gtc atg atg ggc tcc ctc ctg gct gcc acc act gag gcc cct ggc							1260
Thr Val Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly 385		390		395			
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Glu Tyr Phe Phe Ser Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met 400		405		410			
ggt tct ctt gat gcc atg gac aaa cat ctc agc agc cag aac cga tac							1356
Gly Ser Leu Asp Ala Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr 415		420		425		430	

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 Val Gln Asp Lys Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala  
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 Gly Ile Gln His Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln  
                     465                    470                    475  
  
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 Val Arg Ala Met Thr Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr  
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 Lys Arg Leu Phe \*

ttggggaaaaa aaaagtgaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1707

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 Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln  
                     35                    40                    45  
 Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro  
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 Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr  
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 Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln  
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 Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg  
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 Asp Val Phe Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile  
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 Arg Asp Ile Asp Phe Leu Lys Glu Glu Glu His Asp Arg Phe Leu Glu  
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 Glu Ile Met Thr Lys Arg Glu Asp Leu Val Val Ala Pro Ala Gly Val  
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 Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys  
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 Leu Pro Ile Val Asn Glu Asn Asp Glu Leu Val Ala Ile Ile Ala Arg  
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 Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ala  
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Lys	Tyr	Arg	Leu	Asp	Leu	Leu	Ala	Leu	Ala	Gly	Val	Asp	Val	Val	Val
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Leu	Asp	Ser	Ser	Gln	Gly	Asn	Ser	Ile	Phe	Gln	Ile	Asn	Met	Ile	Lys
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Tyr	Ile	Lys	Glu	Lys	Tyr	Pro	Ser	Leu	Gln	Val	Ile	Gly	Gly	Asn	Val
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Val	Thr	Ala	Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	Asp	Ala
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Leu	Arg	Val	Gly	Met	Gly	Ser	Gly	Ser	Ile	Cys	Ile	Ile	Gln	Glu	Val
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Leu	Ala	Cys	Gly	Arg	Pro	Gln	Ala	Thr	Ala	Val	Tyr	Lys	Val	Tyr	Glu
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Tyr	Ala	Arg	Arg	Phe	Gly	Val	Pro	Val	Ile	Ala	Asp	Gly	Gly	Ile	Gln
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Asn	Val	Gly	His	Ile	Ala	Lys	Ala	Leu	Ala	Leu	Gly	Ala	Ser	Thr	Val
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Met	Met	Gly	Ser	Leu	Leu	Ala	Ala	Thr	Thr	Glu	Ala	Pro	Gly	Glu	Tyr
385				390						395					400
Phe	Phe	Ser	Asp	Gly	Ile	Arg	Leu	Lys	Lys	Tyr	Arg	Gly	Met	Gly	Ser
			405						410				415		
Leu	Asp	Ala	Met	Asp	Lys	His	Leu	Ser	Ser	Gln	Asn	Arg	Tyr	Phe	Ser
			420					425					430		
Glu	Ala	Asp	Lys	Ile	Lys	Val	Ala	Gln	Gly	Val	Ser	Gly	Ala	Val	Gln
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Asp	Lys	Gly	Ser	Ile	His	Lys	Phe	Val	Pro	Tyr	Leu	Ile	Ala	Gly	Ile
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Gln	His	Ser	Cys	Gln	Asp	Ile	Gly	Ala	Lys	Ser	Leu	Thr	Gln	Val	Arg
465				470						475					480
Ala	Met	Thr	Tyr	Ser	Gly	Glu	Leu	Lys	Phe	Glu	Lys	Arg	Thr	Ser	Ser
				485					490					495	
Ala	Gln	Val	Glu	Gly	Gly	Val	His	Ser	Leu	His	Ser	Tyr	Glu	Lys	Arg
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<220>  
 <223> Description of Artificial Sequence: Sequence of pMG  
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<220>  
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38

<210> 39

<211> 39

<212> DNA

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<223> Description of Artificial Sequence: Reverse primer for S351Y mutation of hIMPDH type II cDNA

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39